

SEARCH:

Title: US-10-590-810-26_COPY_13_555
 Perfect score: 2763
 Sequence: 1 SPKALEEAPWPPEGAFVGF.....LAVPLEVEVGIGEDWLSAKE 543

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 12150526 seqs, 2531973831 residues

Total number of hits satisfying chosen parameters: 12150526

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2763	100.0	543	27	US-09-791-537-91889	Sequence 91889, A
2	2763	100.0	544	39	US-10-917-157-2	Sequence 2, Appli
3	2763	100.0	544	39	US-10-917-157A-2	Sequence 2, Appli
4	2763	100.0	544	39	US-10-917-157B-2	Sequence 2, Appli
5	2763	100.0	545	39	US-10-917-157-4	Sequence 4, Appli
6	2763	100.0	545	39	US-10-917-157A-4	Sequence 4, Appli
7	2763	100.0	545	39	US-10-917-157B-4	Sequence 4, Appli
8	2763	100.0	552	25	US-09-506-153-1	Sequence 1, Appli
9	2763	100.0	552	32	US-10-216-682-1	Sequence 1, Appli
10	2763	100.0	554	1	PCT-US07-78571-3	Sequence 3, Appli
11	2763	100.0	554	12	US-08-202-032A-6	Sequence 6, Appli
12	2763	100.0	554	19	US-08-931-818-6	Sequence 6, Appli
13	2763	100.0	554	38	US-10-850-816-2	Sequence 2, Appli
14	2763	100.0	554	52	US-12-254-969B-6	Sequence 6, Appli
15	2763	100.0	554	53	US-12-330-201A-2	Sequence 2, Appli
16	2763	100.0	554	54	US-12-441-521A-3	Sequence 3, Appli
17	2763	100.0	558	39	US-10-917-157-5	Sequence 5, Appli
18	2763	100.0	558	39	US-10-917-157A-5	Sequence 5, Appli
19	2763	100.0	558	39	US-10-917-157B-5	Sequence 5, Appli
20	2763	100.0	562	25	US-09-506-153-7	Sequence 7, Appli
21	2763	100.0	562	32	US-10-216-682-7	Sequence 7, Appli
22	2763	100.0	562	35	US-10-590-810-26	Sequence 26, Appl
23	2763	100.0	605	43	US-11-327-195-44	Sequence 44, Appl
24	2763	100.0	605	43	US-11-327-195A-44	Sequence 44, Appl
25	2763	100.0	605	43	US-11-327-195B-44	Sequence 44, Appl

26	2763	100.0	605	43	US-11-327-845-43	Sequence 43, Appl
27	2763	100.0	606	43	US-11-327-195-41	Sequence 41, Appl
28	2763	100.0	606	43	US-11-327-195A-41	Sequence 41, Appl
29	2763	100.0	606	43	US-11-327-195B-41	Sequence 41, Appl
30	2763	100.0	606	43	US-11-327-845-40	Sequence 40, Appl
31	2763	100.0	625	43	US-11-327-195-43	Sequence 43, Appl
32	2763	100.0	625	43	US-11-327-195A-43	Sequence 43, Appl
33	2763	100.0	625	43	US-11-327-195B-43	Sequence 43, Appl
34	2763	100.0	625	43	US-11-327-845-42	Sequence 42, Appl
35	2763	100.0	626	43	US-11-327-195-40	Sequence 40, Appl
36	2763	100.0	626	43	US-11-327-195A-40	Sequence 40, Appl
37	2763	100.0	626	43	US-11-327-195B-40	Sequence 40, Appl
38	2763	100.0	626	43	US-11-327-845-39	Sequence 39, Appl
39	2763	100.0	632	1	PCT-US03-32954-4	Sequence 4, Appli
40	2763	100.0	632	1	PCT-US03-32954-6	Sequence 6, Appli
41	2763	100.0	632	1	PCT-US03-32954-8	Sequence 8, Appli
42	2763	100.0	632	32	US-10-256-705-4	Sequence 4, Appli
43	2763	100.0	632	32	US-10-280-139-4	Sequence 4, Appli
44	2763	100.0	632	32	US-10-280-139-6	Sequence 6, Appli
45	2763	100.0	632	32	US-10-280-139-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-791-537-91889

; Sequence 91889, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS AND

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 91889

; LENGTH: 543

; TYPE: PRT

; ORGANISM: pdb 1KTQ

US-09-791-537-91889

Query Match 100.0%; Score 2763; DB 27; Length 543;

Best Local Similarity 100.0%;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	SPKALEEAPWPPPEGAFVGFVLSRKEPMWADLLALAAAGGRVHRAPEPYKALRDLKEAR	60
Db	1	SPKALEEAPWPPPEGAFVGFVLSRKEPMWADLLALAAAGGRVHRAPEPYKALRDLKEAR	60
Qy	61	GLLAKDLSVLALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALS	120
Db	61	GLLAKDLSVLALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALS	120

Qy 121 ERLFANLWGRLEGEERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIAR 180
 Db 121 ERLFANLWGRLEGEERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIAR 180

Qy 181 LEAEVFRLAGHPFNLSRDQLERVLFDLGLPAIGKTEKTGKRSTSAAVLEALREAHPIV 240
 Db 181 LEAEVFRLAGHPFNLSRDQLERVLFDLGLPAIGKTEKTGKRSTSAAVLEALREAHPIV 240

Qy 241 EKILQYRELTKLKSTYIDPLPDLIHPRTGRHLTRFNQTATATGRLSDDPNLQNIPIVPT 300
 Db 241 EKILQYRELTKLKSTYIDPLPDLIHPRTGRHLTRFNQTATATGRLSDDPNLQNIPIVPT 300

Qy 301 LGQRRIRAFIAEEGWLLVALDYSQIELRVLAHLSGDNELIRVFQEGRDIHTETASWMFGV 360
 Db 301 LGQRRIRAFIAEEGWLLVALDYSQIELRVLAHLSGDNELIRVFQEGRDIHTETASWMFGV 360

Qy 361 PREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAQAFIERFQSFPKVRAWIEK 420
 Db 361 PREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAQAFIERFQSFPKVRAWIEK 420

Qy 421 TLEEGRRRGYVETLFGRRRYVPDLEARVKSVERAAERMAFNMVPGQTAAADLMKLMVVKLF 480
 Db 421 TLEEGRRRGYVETLFGRRRYVPDLEARVKSVERAAERMAFNMVPGQTAAADLMKLMVVKLF 480

Qy 481 PRLEEMGARMLLQVHDELVLEAPKRAEAVARLAKEVMGEGYVPLAVPVEVEVGIGEDWLS 540
 Db 481 PRLEEMGARMLLQVHDELVLEAPKRAEAVARLAKEVMGEGYVPLAVPVEVEVGIGEDWLS 540

Qy 541 AKE 543
 Db 541 AKE 543

21
 1688
 DNA
 Thermus aquaticus

CDS
 (3)..(1688)

21
 cc atg gcc tct ggt ggc ggt ggc tgt ggt ggc ggt ggc agc ccc aag 47
 Met Ala Ser Gly Gly Gly Cys Gly Gly Gly Ser Pro Lys
 1 5 10 15
 gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa ggg gcc ttc gtg gcc 95
 Ala Leu Glu Glu Ala Pro Trp Pro Pro Glu Gly Ala Phe Val Gly
 20 25 30
 ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc gat ctt ctg gcc ctg 143
 Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu
 35 40 45
 gcc gcc gcc agg ggg ggc cgg gtc cac ccg gcc ccc gag cct tat aaa 191
 Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys
 50 55 60
 gcc ctc agg gac ctg aag gag gcg ccg ggg ctt ctc gcc aaa gac ctg 239
 Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu
 65 70 75
 agc gtt ctg gcc ctg agg gaa ggc ctt gcc ctc ccg ccc gcc gac gac 287

Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp	85 90 95	
ccc atg ctc ctc gcc tac ctc ctg gac cct tcc aac acc acc ccc gag	100 105 110	335
Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Gly		
ggg gtg gcc cgg cgc tac gcc ggg gag tgg acg gag gag cgc ggg gag	115 120 125	383
Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu		
cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac ctg tgg ggg agg ctt	130 135 140	431
Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu		
gag ggg gag gag agg ctc ctt tgg ctt tac cgg gag gtg gag agg ccc	145 150 155	479
Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro		
ctt tcc gct gtc ctg gcc cac atg gag gcc acg ggg gtg cgc ctg gac	160 165 170 175	527
Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp		
gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg gcc gag atc gcc	180 185 190	575
Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala		
cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc cac ccc ttc aac ctc	195 200 205	623
Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu		
aac tcc cgg gac cag ctg gaa agg gtc ctc ttt gac gag cta ggg ctt	210 215 220	671
Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu		
ccc gcc atc gcc aag acg gag aag acc gcc aag cgc tcc acc agc gcc	225 230 235	719
Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala		
gcc gtc ctg ggg gcc ctc cgc gag gcc cac ccc atc gtg gag aag atc	240 245 250 255	767
Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile		
ctg cag tac cgg gag ctc acc aag ctg aag agc acc tac att gac ccc	260 265 270	815
Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro		
ttg ccg gac ctc atc cac ccc agg acg ggc cgc ctc cac acc cgc ttc	275 280 285	863
Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe		
aac cag acg gcc acg gcc acg ggc agg cta agt agc tcc gat ccc aac	290 295 300	911
Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Asp Pro Asn		
ctc cag aac atc ccc gtc cgc acc ccg ctt ggg cag agg atc cgc cgg	305 310 315	959
Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg		
gcc ttc atc gcc gag gag ggg tgg cta ttg gtg acc ctg gac tat agc	320 325 330 335	1007
Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Thr Leu Asp Tyr Ser		
cag ata gag ctc agg gtg ctg gcc cac ctc tcc ggc gac gag aac ctg	340 345 350	1055
Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu		
atc cgg gtc ttc cag gag ggg cgg gac atc cac acg gag acc gcc agc	355 360 365	1103
Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Thr Ala Ser		
tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac ccc ctg atg cgc cgg	370 375 380	1151
Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg		
gcg gcc aag acc atc aac ttc ggg gtc ctc tac gcc atg tgc gcc cac	385 390 395	1199
Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His		
arg ctc tcc cag gag cta gcc atc cct tac gag gag gcc cag gcc ttc	400 405 410 415	1247
Cgc Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe		
att gag cgc tac ttt cag agc ttc ccc aag gtg cgg gcc tgg att gag		1295

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Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu
420 425 430
aag acc ctg gag gag ggc agg agg cgg ggg tac gtg gag acc ctc ttc 1343
Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe
435 440 445
ggc cgc cgc cgc tac gtg cca gac cta gag gcc cgg gtg aag agc gtg 1391
Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val
450 455 460
cgg gag gcg gcc gag cgc atg gcc ttc aac atg ccc gtc cag gcc acc 1439
Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr
465 470 475
gcc gcc gac ctc atg aag ctg gct atg gtg aag ctc ttc ccc agg ctg 1487
Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu
480 485 490 495
gag gaa atg ggg gcc agg atg ctc ctt cag gtc cac gac gag ctg gtc 1535
Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val
500 505 510
ctc gag gcc cca aaa gag ggg gcg gag gcc gtg gcc cgg ctg gcc aag 1583
Leu Glu Ala Pro Lys Glu Gly Ala Glu Ala Val Ala Arg Leu Ala Lys
515 520 525
gag gtc atg gag ggg gtg tat ccc ctg gcc gtg ccc ctg gag gtg gag 1631
Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu
530 535 540
gtg ggg ata ggg gag gac agg ctc tcc gcc aag gag gcg gcc gca ctg 1679
Val Gly Ile Gly Glu Asp Arg Leu Ser Ala Lys Glu Ala Ala Leu
545 550 555
gtg ccg cgc 1688
Val Pro Arg
560

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W550 tryptophan

SEQ ID NO:26 is Thermus aquaticus

EAST SEARCH:

US 7488816 11/065,943 (Wilder exmnr)

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IS&R L1 1 ("7417133").PN.US-PGPUB; USPAT; USOCR 2010/07/12 10:22
BRS L3 16 W550 USPAT 2010/07/12 10:31
BRS L4 62051 polymerase USPAT 2010/07/12 10:35
BRS L5 17552 14 and tryptophan USPAT 2010/07/12 10:35
BRS L6 561 14 and tryptophan.clm. USPAT 2010/07/12 10:36
BRS L7 4440 "550".clm. USPAT 2010/07/12 10:56
BRS L8 108 14 and 17 USPAT 2010/07/12 10:57

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d his

(FILE 'HOME' ENTERED AT 11:32:56 ON 12 JUL 2010)

FILE 'MEDLINE, CAPLUS, BIOSIS, BIOTECHNO, EMBASE, JAPIO' ENTERED AT
11:36:07 ON 12 JUL 2010

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L1 1642496 S POLYMERASE
L2 0 S L1 AND W550
L3 4979 S L1 AND TRYPTOPHAN
L4 3 S L3 AND 550

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L5 1522 S L1 AND 550
L6 2207 S L3 AND (MUTA? OR VARIAN? OR SUBSTIT?)
L7 12 S L6 AND TAQ
L8 8 DUP REM L7 (4 DUPLICATES REMOVED)

FILE 'MEDLINE, BIOSIS, CAPLUS, BIOTECHNO, EMBASE, JAPIO' ENTERED AT
13:52:04 ON 12 JUL 2010
L9 1642496 S POLYMERASE
L10 245 S L9 AND 827
L11 0 S L10 AND TRYPTOPHAN
L12 2 S L10 AND TAQ
L8 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2004:1/1780 CAPLUS
DN 140:351362

TI A novel strategy to engineer DNA polymerases for enhanced processivity and improved performance in vitro
AU Wang, Yan; Prosen, Dennis E.; Mei, Li; Sullivan, John C.; Finney, Michael; Vander Horn, Peter B.
CS Department of Research and Development, MJ Bioworks Inc., South San Francisco, CA, 94080, USA
SO Nucleic Acids Research (2004), 32(3), 1197-1207
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB Mechanisms that allow replicative DNA polymerases to attain high processivity are often specific to a given polymerase and cannot be generalized to others. Here the authors report a protein engineering-based approach to significantly improve the processivity of DNA polymerases by covalently linking the polymerase domain to a sequence non-specific dsDNA binding protein. Using Sso7d from Sulfolobus solfataricus as the DNA binding protein, the authors demonstrate that the processivity of both family A and family B polymerases can be significantly enhanced. By introducing point mutations in Sso7d, the authors show that the dsDNA binding property of Sso7d is essential for the enhancement. The authors present evidence supporting two novel conclusions. First, the fusion of a heterologous dsDNA binding protein to a polymerase can increase processivity without compromising catalytic activity and enzyme stability. Second, polymerase processivity is limiting for the efficiency of PCR, such that the fusion enzymes exhibit profound advantages over unmodified enzymes in PCR applications. This technol. has the potential to broadly improve the performance of nucleic acid modifying enzymes.
OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (27 CITINGS)
RE.CNT 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT